

SEQUENCE LISTING

<110> Giger, Roman J.

<120> IDENTIFICATION OF NOVEL NOGO-RECEPTORS
AND METHODS RELATED THERETO

<130> 21108.0028U2

<140> 10/551,833
<141> 2005-10-03

<150> PCT/US04/010328
<151> 2004-04-02

<150> 60/460,849
<151> 2003-04-04

<160> 29

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 1
Met Lys Arg Ala Ser Ser Gly Gly Ser Arg Leu Leu Ala Trp Val Leu
1 5 10 15
Trp Leu Gln Ala Trp Arg Val Ala Thr Pro Cys Pro Gly Ala Cys Val
20 25 30
Cys Tyr Asn Glu Pro Lys Val Thr Thr Ser Cys Pro Gln Gln Gly Leu
35 40 45
Gln Ala Val Pro Thr Gly Ile Pro Ala Ser Ser Gln Arg Ile Phe Leu
50 55 60
His Gly Asn Arg Ile Ser Tyr Val Pro Ala Ala Ser Phe Gln Ser Cys
65 70 75 80
Arg Asn Leu Thr Ile Leu Trp Leu His Ser Asn Ala Leu Ala Gly Ile
85 90 95
Asp Ala Ala Ala Phe Thr Gly Leu Thr Leu Leu Glu Gln Leu Asp Leu
100 105 110
Ser Asp Asn Ala Gln Leu Arg Val Val Asp Pro Thr Thr Phe Arg Gly
115 120 125
Leu Gly His Leu His Thr Leu His Leu Asp Arg Cys Gly Leu Gln Glu
130 135 140
Leu Gly Pro Gly Leu Phe Arg Gly Leu Ala Ala Leu Gln Tyr Leu Tyr
145 150 155 160
Leu Gln Asp Asn Asn Leu Gln Ala Leu Pro Asp Asn Thr Phe Arg Asp
165 170 175

Leu Gly Asn Leu Thr His Leu Phe Leu His Gly Asn Arg Ile Pro Ser
 180 185 190
 Val Pro Glu His Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu
 195 200 205
 Leu His Gln Asn His Val Ala Arg Val His Pro His Ala Phe Arg Asp
 210 215 220
 Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu Ser Met
 225 230 235 240
 Leu Pro Ala Glu Val Leu Val Pro Leu Arg Ser Leu Gln Tyr Leu Arg
 245 250 255
 Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro Leu Trp
 260 265 270
 Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Glu Val Pro Cys Asn
 275 280 285
 Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg Leu Ala Ala Ser
 290 295 300
 Asp Leu Glu Gly Cys Ala Val Ala Ser Gly Pro Phe Arg Pro Phe Gln
 305 310 315 320
 Thr Asn Gln Leu Thr Asp Glu Glu Leu Leu Gly Leu Pro Lys Cys Cys
 325 330 335
 Gln Pro Asp Ala Ala Asp Lys Ala Ser Val Leu Glu Pro Gly Arg Pro
 340 345 350
 Ala Ser Ala Gly Asn Ala Leu Lys Gly Arg Val Pro Pro Gly Asp Thr
 355 360 365
 Pro Pro Gly Asn Gly Ser Gly Pro Arg His Ile Asn Asp Ser Pro Phe
 370 375 380
 Gly Thr Leu Pro Gly Ser Ala Glu Pro Pro Leu Thr Ala Leu Arg Pro
 385 390 395 400
 Gly Gly Ser Glu Pro Pro Gly Leu Pro Thr Thr Gly Pro Arg Arg Arg
 405 410 415
 Pro Gly Cys Ser Arg Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly
 420 425 430
 Gln Ala Gly Ser Gly Ser Ser Gly Thr Gly Asp Ala Glu Gly Ser Gly
 435 440 445
 Ala Leu Pro Ala Leu Ala Cys Ser Leu Ala Pro Leu Gly Leu Ala Leu
 450 455 460
 Val Leu Trp Thr Val Leu Gly Pro Cys
 465 470

<210> 2
 <211> 286
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

<400> 2
 Pro Val Thr Pro Ser Cys Pro Met Leu Cys Thr Cys Tyr Ser Ser Pro
 1 5 10 15
 Pro Thr Val Ser Cys Gln Ala Asn Asn Phe Ser Ser Val Pro Leu Ser
 20 25 30
 Leu Pro Pro Ser Thr Gln Arg Leu Phe Leu Gln Asn Asn Leu Ile Arg
 35 40 45
 Ser Leu Arg Pro Gly Thr Phe Gly Pro Asn Leu Leu Thr Leu Trp Leu
 50 55 60

Phe Ser Asn Asn Leu Ser Thr Ile Tyr Pro Gly Thr Phe Arg His Leu
 65 70 75 80
 Gln Ala Leu Glu Glu Leu Asp Leu Gly Asp Asn Arg His Leu Arg Ser
 85 90 95
 Leu Glu Pro Asp Thr Phe Gln Gly Leu Glu Arg Leu Gln Ser Leu His
 100 105 110
 Leu Tyr Arg Cys Gln Leu Ser Ser Leu Pro Gly Asn Ile Phe Arg Gly
 115 120 125
 Leu Val Ser Leu Gln Tyr Leu Tyr Leu Gln Glu Asn Ser Leu Leu His
 130 135 140
 Leu Gln Asp Asp Leu Phe Ala Asp Leu Ala Asn Leu Ser His Leu Phe
 145 150 155 160
 Leu His Gly Asn Arg Leu Arg Leu Leu Thr Glu His Val Phe Arg Gly
 165 170 175
 Leu Gly Ser Leu Asp Arg Leu Leu Leu His Gly Asn Arg Leu Gln Gly
 180 185 190
 Val His Arg Ala Ala Phe His Gly Leu Ser Arg Leu Thr Ile Leu Tyr
 195 200 205
 Leu Phe Asn Asn Ser Leu Ala Ser Leu Pro Gly Glu Ala Leu Ala Asp
 210 215 220
 Leu Pro Ala Leu Glu Phe Leu Arg Leu Asn Ala Asn Pro Trp Ala Cys
 225 230 235 240
 Asp Cys Arg Ala Arg Pro Leu Trp Ala Trp Phe Gln Arg Ala Arg Val
 245 250 255
 Ser Ser Ser Asp Val Thr Cys Ala Thr Pro Pro Glu Arg Gln Gly Arg
 260 265 270
 Asp Leu Arg Thr Leu Arg Asp Thr Asp Phe Gln Ala Cys Pro
 275 280 285

<210> 3
 <211> 420
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

<400> 3
 Met Leu Pro Gly Leu Arg Arg Leu Leu Gln Gly Pro Ala Ser Ala Cys
 1 5 10 15
 Leu Leu Leu Thr Leu Leu Ala Leu Pro Pro Val Thr Pro Ser Cys Pro
 20 25 30
 Met Leu Cys Thr Cys Tyr Ser Ser Pro Pro Thr Val Ser Cys Gln Ala
 35 40 45
 Asn Asn Phe Ser Ser Val Pro Leu Ser Leu Pro Pro Ser Thr Gln Arg
 50 55 60
 Leu Phe Leu Gln Asn Asn Leu Ile Arg Ser Leu Arg Pro Gly Thr Phe
 65 70 75 80
 Gly Pro Asn Leu Leu Thr Leu Trp Leu Phe Ser Asn Asn Leu Ser Thr
 85 90 95
 Ile Tyr Pro Gly Thr Phe Arg His Leu Gln Ala Leu Glu Glu Leu Asp
 100 105 110
 Leu Gly Asp Asn Arg His Leu Arg Ser Leu Glu Pro Asp Thr Phe Gln
 115 120 125
 Gly Leu Glu Arg Leu Gln Ser Leu His Leu Tyr Arg Cys Gln Leu Ser
 130 135 140

Ser Leu Pro Gly Asn Ile Phe Arg Gly Leu Val Ser Leu Gln Tyr Leu
 145 150 155 160
 Tyr Leu Gln Glu Asn Ser Leu Leu His Leu Gln Asp Asp Leu Phe Ala
 165 170 175
 Asp Leu Ala Asn Leu Ser His Leu Phe Leu His Gly Asn Arg Leu Arg
 180 185 190
 Leu Leu Thr Glu His Val Phe Arg Gly Leu Gly Ser Leu Asp Arg Leu
 195 200 205
 Leu Leu His Gly Asn Arg Leu Gln Gly Val His Arg Ala Ala Phe His
 210 215 220
 Gly Leu Ser Arg Leu Thr Ile Leu Tyr Leu Phe Asn Asn Ser Leu Ala
 225 230 235 240
 Ser Leu Pro Gly Glu Ala Leu Ala Asp Leu Pro Ala Leu Glu Phe Leu
 245 250 255
 Arg Leu Asn Ala Asn Pro Trp Ala Cys Asp Cys Arg Ala Arg Pro Leu
 260 265 270
 Trp Ala Trp Phe Gln Arg Ala Arg Val Ser Ser Ser Asp Val Thr Cys
 275 280 285
 Ala Thr Pro Pro Glu Arg Gln Gly Arg Asp Leu Arg Thr Leu Arg Asp
 290 295 300
 Thr Asp Phe Gln Ala Cys Pro Pro Pro Thr Pro Thr Arg Pro Gly Ser
 305 310 315 320
 Arg Ala Arg Gly Asn Ser Ser Ser Asn His Leu Tyr Gly Val Ala Glu
 325 330 335
 Ala Gly Ala Pro Pro Ala Asp Pro Ser Thr Leu Tyr Arg Asp Leu Pro
 340 345 350
 Ala Glu Asp Ser Arg Gly Arg Gln Gly Gly Asp Ala Pro Thr Glu Asp
 355 360 365
 Asp Tyr Trp Gly Gly Tyr Gly Gly Glu Asp Gln Arg Gly Glu Gln Thr
 370 375 380
 Cys Pro Gly Ala Ala Cys Gln Ala Pro Ala Asp Ser Arg Gly Pro Val
 385 390 395 400
 Leu Ser Ala Gly Leu Arg Thr Pro Leu Leu Cys Leu Leu Leu Leu Ala
 405 410 415
 Pro His His Leu
 420

<210> 4
 <211> 175
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

<400> 4
 Asn Gly Asn Ala Trp Asp Cys Gly Cys Arg Ala Arg Ser Leu Trp Glu
 1 5 10 15
 Trp Leu Arg Arg Phe Arg Gly Ser Ser Ser Val Val Pro Cys Ala Thr
 20 25 30
 Pro Glu Leu Arg Gln Gly Gln Asp Leu Lys Ser Leu Arg Val Glu Asp
 35 40 45
 Phe Arg Asn Cys Thr Gly Pro Ala Ser Pro His Gln Ile Lys Ser His
 50 55 60
 Thr Leu Ser Thr Ser Asp Arg Ala Ala Arg Lys Glu His His Pro Ser
 65 70 75 80

His	Gly	Ala	Ser	Arg	Asp	Lys	Gly	His	Pro	His	Gly	His	Leu	Pro	Gly
				85					90						95
Ser	Arg	Ser	Gly	Ser	Lys	Lys	Pro	Gly	Lys	Asn	Cys	Thr	Ser	His	Arg
															100
									105						110
Asn	Arg	Asn	Gln	Ile	Ser	Lys	Gly	Ser	Ala	Gly	Lys	Glu	Leu	Pro	Glu
															115
									120						125
Leu	Gln	Asp	Tyr	Ala	Pro	Asp	Tyr	Gln	His	Lys	Phe	Ser	Phe	Asp	Ile
															130
									135						140
Met	Pro	Thr	Ala	Arg	Pro	Lys	Arg	Lys	Gly	Lys	Cys	Ala	Arg	Arg	Thr
															145
									150		155				160
Pro	Ile	Arg	Ala	Pro	Ser	Gly	Val	Gln	Gln	Ala	Ser	Ser	Gly	Thr	
															165
									170						175

<210> 5

<211> 445

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 5

Met	Leu	Arg	Lys	Gly	Cys	Cys	Val	Glu	Leu	Leu	Leu	Leu	Leu	Leu	Ala
									1	5	10				15
Gly	Glu	Leu	Pro	Leu	Ser	Gly	Gly	Cys	Pro	Arg	Asp	Cys	Val	Cys	Tyr
									20	25					30
Pro	Ser	Pro	Met	Thr	Val	Ser	Cys	Gln	Ala	His	Asn	Phe	Ala	Ala	Ile
									35	40					45
Pro	Glu	Gly	Ile	Pro	Glu	Asp	Ser	Glu	Arg	Ile	Phe	Leu	Gln	Asn	Asn
									50	55					60
His	Ile	Thr	Phe	Leu	Gln	Gln	Gly	His	Phe	Ser	Pro	Ala	Met	Val	Thr
									65	70					80
Leu	Trp	Ile	Tyr	Ser	Asn	Asn	Ile	Thr	Phe	Ile	Ala	Pro	Asn	Thr	Phe
									85	90					95
Glu	Gly	Phe	Val	His	Leu	Glu	Leu	Asp	Leu	Gly	Asp	Asn	Arg	Gln	
									100	105					110
Leu	Arg	Thr	Leu	Ala	Pro	Glu	Thr	Phe	Gln	Gly	Leu	Val	Lys	Leu	His
									115	120					125
Ala	Leu	Tyr	Leu	Tyr	Lys	Cys	Gly	Leu	Ser	Ser	Leu	Pro	Ala	Gly	Ile
									130	135					140
Phe	Gly	Gly	Leu	His	Ser	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	His
									145	150					160
Ile	Glu	Tyr	Leu	Gln	Asp	Asp	Ile	Phe	Val	Asp	Leu	Val	Asn	Leu	Ser
									165	170					175
His	Leu	Phe	Leu	His	Gly	Asn	Lys	Leu	Trp	Ser	Leu	Gly	Gln	Gly	Ile
									180	185					190
Phe	Arg	Gly	Leu	Val	Asn	Leu	Asp	Arg	Leu	Leu	Leu	His	Glu	Asn	Gln
									195	200					205
Leu	Gln	Trp	Val	His	His	Lys	Ala	Phe	His	Asp	Leu	His	Arg	Leu	Thr
									210	215					220
Thr	Leu	Phe	Leu	Phe	Asn	Asn	Ser	Leu	Thr	Glu	Leu	Gln	Gly	Asp	Cys
									225	230					240
Leu	Ala	Pro	Leu	Val	Ala	Leu	Glu	Phe	Leu	Arg	Leu	Asn	Gly	Asn	Ala
									245	250					255
Trp	Asp	Cys	Gly	Cys	Arg	Ala	Arg	Ser	Leu	Trp	Glu	Trp	Leu	Arg	Arg
									260	265					270

Phe Arg Gly Ser Ser Ser Val Val Pro Cys Ala Thr Pro Glu Leu Arg
 275 280 285
 Gln Gly Gln Asp Leu Lys Ser Leu Arg Val Glu Asp Phe Arg Asn Cys
 290 295 300
 Thr Gly Pro Ala Ser Pro His Gln Ile Lys Ser His Thr Leu Ser Thr
 305 310 315 320
 Ser Asp Arg Ala Ala Arg Lys Glu His His Pro Ser His Gly Ala Ser
 325 330 335
 Arg Asp Lys Gly His Pro His Gly His Leu Pro Gly Ser Arg Ser Gly
 340 345 350
 Ser Lys Lys Pro Gly Lys Asn Cys Thr Ser His Arg Asn Arg Asn Gln
 355 360 365
 Ile Ser Lys Gly Ser Ala Gly Lys Glu Leu Pro Glu Leu Gln Asp Tyr
 370 375 380
 Ala Pro Asp Tyr Gln His Lys Phe Ser Phe Asp Ile Met Pro Thr Ala
 385 390 395 400
 Arg Pro Lys Arg Lys Gly Lys Cys Ala Arg Arg Thr Pro Ile Arg Ala
 405 410 415
 Pro Ser Gly Val Gln Gln Ala Ser Ser Gly Thr Ala Leu Gly Val Ser
 420 425 430
 Leu Leu Ala Trp Ile Leu Gly Leu Val Val Ser Leu Arg
 435 440 445

<210> 6
<211> 2215
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 6

tcgcggacac	ggggcgcacg	gaccgaccga	ctaaccgact	ccctgcgggt	ctgcgctgcc	60
gagggggcgcg	gacaccggtt	gtccagggtc	aacctcagccc	tttccatctc	gtcggtcccc	120
gccccgtccc	gtcggggccc	atggctcctt	cagaggcaca	gagtccgggg	ggcgcaagggt	180
agagctccgc	agccccccta	cgtagccccg	gactcccggg	tccttacgg	gccccgcgga	240
gtccccgcgg	tctgtccggc	gggataaggg	agcgagtggg	agcgccctcc	ccccccgcgc	300
gccccctccc	ccgatcgctg	agacaagatg	ctgcccgggc	tccggcgcct	gtcgcaaggt	360
cctgcctcag	cctgcctcct	gctgacactc	ctggccctcc	ctcctgtgac	ccccagctgc	420
cctatgtct	gcacctgcta	ctcctctccg	cccacagtga	gctgccaggc	caacaacttc	480
tcctcggtgc	cgctgtcctt	gccacccagt	acacagcgac	tcttcttgca	gaacaacctc	540
attcgctcac	tgcggccagg	aacttttggg	ccaaacctgc	tcaccctgtg	gctcttctcc	600
aacaacctct	ccaccatcta	ccctggcacc	ttccggccatc	tgcaggccct	agaggaactg	660
gacctcggtg	acaatcgga	cctgcgctcc	ctggagcctg	acacattcca	gggcctggag	720
aggctgcagt	cactacatct	gtaccgggtc	cagctcagca	gtctgcctgg	caacatcttc	780
cgaggcctgg	tcagcctaca	gtacccctac	ctccaggaga	acagcctgtct	ccacacctacag	840
gatgacttgt	tgcggcacc	ggccaacctg	agccaccttt	tcctccacgg	gaaccgcctg	900
cggctgctca	cggagcacgt	gttccggcgg	ttggggcagcc	tggaccggct	gctgctgcac	960
gggaacccggc	tgcagggcgt	acaccgcgca	gccttccacg	gtctcagccg	cctcaccatc	1020
ctttaacctgt	tcaacaacag	cctggcctcg	ctgccccggag	aggcgctggc	tgacactgcca	1080
gcgctcgagt	tcctgcggct	caacgccaac	ccctggcggt	gcgactgccc	cgctcgcccg	1140
ctctgggctt	ggttccagcg	cgcgcgggt	tccagctccg	acgtgacctg	cgccaccccg	1200
cccgagcgcc	agggccggga	cctgcgcacg	ctgcgcgaca	ccgatttcca	agcgtgccc	1260
ccgccccacac	ccacgcggcc	ggcagccgc	gccccggca	acagctcttc	caaccacctg	1320
tacggcgtgg	ccgaggcggg	cgctcccccc	gcagacccat	ccacgctcta	ccgagacctg	1380
cccccggagg	actcgcgggg	gctgcaggc	ggggacgcgc	ccactgagga	cgactactgg	1440

gggggctacg	gcggcgagga	ccagcgaggc	gagcagacgt	gtcccggggc	cgcgtgccag	1500
gcgcggcg	actcgctgg	ccccgtgtc	tcggccggc	tgcgcacccc	tctgctctgc	1560
ctcttgc	ttggctccca	tcacctctga	ctgcgggt	ccgatggaag	agaccacgtt	1620
cttcggcc	ctccccctt	ctgccccacg	gagctgaggc	tccgaacttg	ccccttgttt	1680
gcgacccggc	ctggcacctt	cccttaggc	cctcgctt	tttcttcccc	tgaccaggct	1740
gcctcattt	ccttccgggc	tgttgtact	tatgtatggc	agccccctaag	acggtgtata	1800
aggtgttcg	gccccattcg	ccctgattct	agacattaac	tcttctgccc	ccatccaaag	1860
gctggggcgt	gacacccag	gcagccgtt	ctcctcttc	ccccggccca	cagtggactc	1920
ggaggggctt	tttgtccgca	gagcaccttc	caccaggaga	gcctttgaaa	gtccccctg	1980
ggagccccc	ctccctcccc	tttggaggga	tgtctcagcg	aggcccaggc	tgccccctgga	2040
ccctgcttgt	cctgatccct	tcagcctcct	gacacccggag	aatacttttc	tcctaagtct	2100
accaggaca	cttttttaggt	gcctggagag	atttcctctc	accatggccc	ctgtgtggtg	2160
aagataaaaag	aaattgtttt	ggggaaaaaa	tttattaaaa	aattctatta	ttttt	2215

<210> 7
<211> 1422
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 7	60					
atgaagaggg	cgtcctccgg	aggaagccgg	ctgctggcat	gggtgttatg	gctacaggcc	60
tggagggtag	caacgcctcg	ccctgggtcc	tgtgtgtgt	acaatgagcc	caaggtcaca	120
acaagctgcc	cccagcaggg	cctgcaggct	gtaccactg	gatcccacg	ctccagccag	180
agaatcttc	tgcacggcaa	ccgaatctct	tacgtgccag	ccgcccagctt	ccagtcatgc	240
cggaatctca	ccatcctgtg	gctgcactca	aatgcgttgg	ccgggatttga	tgccgcggcc	300
ttcaactggc	tgaccctcct	ggagcaacta	gatcttagt	acaatgcaca	gctccgtgtc	360
gtggacccca	ccacgttccg	tggcctgggc	cacctgcaca	cgctgcaccc	agaccgatgc	420
ggcctgcagg	agctggggcc	tggcctattc	cgtggcttgg	cagctctgca	gtacctctac	480
ctacaagaca	acaacctgca	ggcacttccc	gacaacaccc	tccgagaccc	ggcaacaccc	540
acgcacatct	ttctgcatgg	caaccgtatc	cccagtgtt	ctgagcagcc	tttccgtggc	600
ttgcacagtc	ttgaccgtct	cctcttgcac	cagaaccatg	tggctcggt	gcacccacat	660
gcctccggg	accttggccg	actcatgacc	ctctacctgt	ttgccaacaa	cctctccat	720
ctccccgcag	aggtcctagt	gcccctgagg	tctctgcagt	acctgcgact	aatgacaac	780
ccctgggtgt	gtgactgcag	ggcacgtccg	ctctggccct	ggctgcagaa	tttccgaggt	840
tcctcatccg	aggtgcctcg	caacacctcc	caacgcctgg	caggccgtga	tctgaagcgc	900
ctggctgcca	gtgactttaga	gggttgtgt	gtggcttccg	ggcccttccg	tcccttccag	960
accaatcagc	tcactgatga	ggagctgtgt	ggcctcccca	agtgcgtcca	gccggatgt	1020
gcagacaagg	cctcagact	ggaacccggg	aggccggcgt	ctgctggaaa	tgcactcaag	1080
ggacgtgtgc	ctcccggtga	cactccacca	ggcaatggct	caggcccacg	gcacatcaat	1140
gactctccat	ttgggacttt	gccgggctct	gcagagcccc	cactgactgc	cctgcggcct	1200
gggggttccg	agccccccgg	actgcccacc	acgggtcccc	gcaggaggcc	aggttgtcc	1260
agaaaagaacc	gcacccgtag	ccactgcccgt	ctggccagg	caggaagtgg	gaggcgtgg	1320
actggggatg	cagaaggttc	ggggccctg	cctgccttgg	cctgcagcc	tgctcctctg	1380
ggccttgcac	ttgtactttt	gacagtgtt	ggccctgtt	ga		1422

<210> 8
<211> 2601
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<220>
 <221> misc_feature
 <222> (0)...(0)
 <223> n = a, t, c, or g

<400> 8

tgccggccgc	ggcgcttcc	cggagctggg	ctgtgcgtgc	gagcgccctt	ttgcagcagc	60
cgctgcccga	gggggcgggg	aagaggggac	atcggtctgc	cggccagggg	gccccgtccc	120
ccctcaaaac	cgcctgaaa	gtgtttgggg	cggcagaatc	aggccgcccc	ctcggtggag	180
caagccactc	ccccggggc	ttagagagcg	cacggcggttgc	gttggcagcg	ccggcggttgc	240
tagcaggcgc	cgggtccctg	ggccgcgnnc	ttgggctcac	catgccccctg	cgggaccggg	300
ccgcccggca	caagcggatt	cccggttcgc	ccccgcctcg	acgcgcctcg	attagctgta	360
gctggcgccc	agggatttga	atctggaccc	caggagggag	cgcgccttagg	ccgacaccccg	420
aacggcgccc	ccgcggccaa	catgcttcgc	aaagggtgt	gtgtgaaatt	gctgctgttg	480
ctgctggctg	gagagctacc	tctgagtgg	gttgtccctc	gagactgtgt	gtgtctacccc	540
tcgcccattga	ctgtcagttg	ccaggcacac	aacttgcgg	ccatccccca	gggcataccca	600
gaggacagcg	agcgcattt	cctgcagaac	aatcacatca	ccttcctcca	gcagggccac	660
ttcagccccc	ccatggtcac	cctctggatc	tactccaaca	acatcactt	cattgctccc	720
aacacccctt	agggcttgc	gcatctggag	gagctagacc	ttggagacaa	ccggcagctt	780
cgaacgctgg	caccgcagac	cttccaaggc	ctggtaagc	ttcacgcct	ctacctctac	840
aagtgcggac	tgagctccct	gcctgcgggc	atcttggtg	gcctgcacag	cctgcagttac	900
ctctacttgc	aggacaacca	tattgagttac	ctccaagatg	acatctttgt	ggacctggtc	960
aacctcagtc	acttgtttct	ccatggcaac	aagctatgga	gcctgggcca	gggcatacttc	1020
cggggcctgg	tgaacctgga	ccgggttgctg	ctgcatgaga	accagctaca	gtgggtccac	1080
cacaaggctt	tccatgacct	ccacaggcta	accaccctct	ttctcttcaa	caatagcctc	1140
accggagctgc	aggggtgactg	cctggccccc	ctggtgccccc	tggagtttct	tcgcctcaat	1200
gggaatgctt	gggactgtgg	ctgcccggca	cggccctgt	gggaatggct	gcgaagggttc	1260
cgtggctcca	gctctgttgc	ccctgcgcgc	actccagagc	tgcggcaagg	acaggacctg	1320
aagtgcgtga	gggttgagga	cttccggaaac	tgcactggac	cagcgtctcc	tcaccagatc	1380
aagtctcaca	cgcttagcac	ctctgacagg	gctgcccgc	aggagcacca	tccctcccac	1440
ggtgccctca	gggacaaagg	ccacccacat	ggccatctgc	ctggctccag	gtcaggttcc	1500
aagaagccag	gcaagaactg	caccagccac	aggaaccgaa	accagatctc	taaggggagc	1560
gctgggaaag	agcttcctga	actgcaggac	tatgcccccg	actatcagca	caagttcagc	1620
tttgacatca	tgcccactgc	acgacccaag	aggaagggca	agtgtccccg	caggacccccc	1680
atccgtgcc	ccagtgggt	gcagcaggcc	tcctcaaggc	cggccctcgg	ggtctactc	1740
ctggcctgga	tactgggct	ggtgttatct	ctccgctgag	gacccaggc	acggtcaccc	1800
agcaactgcca	cctgtccagc	aaggaaacag	aatctttct	tctttcttt	tctttccctc	1860
taagtggaaag	atctgctggg	tttcaggaaa	aggctctaa	aaccttcagt	ccagtgtgg	1920
ccttttgggt	ggattaaagc	ccaaacggta	agctgttagac	aggaagggga	gcacatctta	1980
cctggctgtc	ctgaccgagc	acctccggac	agtatccac	tcagccagtg	gtcaaaggc	2040
acaccaagtg	agtcgttagt	ggtgtcagga	catgtcccc	ttgaagaaat	gggcttgcgg	2100
aatcctggtc	acttggaaag	aagggtgaa	ggaccctgt	gttttcggaa	ggagcaggac	2160
tcagaacaag	gctcaccctag	agtcagctgg	ggcaaacagc	aatctcagag	cactcttgg	2220
cttgccctgag	atcacttagt	taactggccc	tgtccaaatcc	tatgcctccc	tcagtcctca	2280
cccatgaggg	taatgcctct	cattcctgaa	gtctcaggca	gtcctggcag	acttgctgg	2340
gttcaagaac	caatcaccaa	aggagagatc	gccagaggat	gacatataaga	actttactcg	2400
taatgagagt	cacacagaag	gtgcagttt	atacctatgt	ccacttataat	atatattctc	2460
actctgacca	cacatccaca	taatataat	atataatatta	taaatatata	aatgcacagg	2520
tcccccaacc	cactccttac	caaactgtat	gtcttatcat	gtttataaaac	tatacgggaa	2580
cctaaaaaaaaa	aaaaagtgaa	a				2601

<210> 9
 <211> 445
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 9

Met Leu Arg Lys Gly Cys Cys Val Glu Leu Leu Leu Leu Ala
 1 5 10 15
 Gly Glu Leu Pro Leu Ser Gly Gly Cys Pro Arg Asp Cys Val Cys Tyr
 20 25 30
 Pro Ser Pro Met Thr Val Ser Cys Gln Ala His Asn Phe Ala Ala Val
 35 40 45
 Pro Glu Gly Ile Pro Glu Asp Ser Glu Arg Ile Phe Leu Gln Asn Asn
 50 55 60
 His Ile Thr Phe Leu Gln Gln Gly His Phe Ser Pro Ala Met Val Thr
 65 70 75 80
 Leu Trp Ile Tyr Ser Asn Asn Ile Thr Phe Ile Ala Pro Asn Thr Phe
 85 90 95
 Glu Gly Phe Val His Leu Glu Glu Leu Asp Leu Gly Asp Asn Arg Gln
 100 105 110
 Leu Arg Thr Leu Ala Pro Glu Thr Phe Gln Gly Leu Val Lys Leu His
 115 120 125
 Ala Leu Tyr Leu Tyr Lys Cys Gly Leu Ser Ser Leu Pro Ala Gly Ile
 130 135 140
 Phe Gly Gly Leu His Ser Leu Gln Tyr Leu Tyr Leu Gln Asp Asn His
 145 150 155 160
 Ile Glu Tyr Leu Gln Asp Asp Ile Phe Val Asp Leu Val Asn Leu Ser
 165 170 175
 His Leu Phe Leu His Gly Asn Lys Leu Trp Ser Leu Gly Gln Gly Ile
 180 185 190
 Phe Arg Gly Leu Val Asn Leu Asp Arg Leu Leu His Glu Asn Gln
 195 200 205
 Leu Gln Trp Val His His Lys Ala Phe His Asp Leu His Arg Leu Thr
 210 215 220
 Thr Leu Phe Leu Phe Asn Asn Ser Leu Thr Glu Leu Gln Gly Asp Cys
 225 230 235 240
 Leu Ala Pro Leu Val Ala Leu Glu Phe Leu Arg Leu Asn Gly Asn Ala
 245 250 255
 Trp Asp Cys Gly Cys Arg Ala Arg Ser Leu Trp Glu Trp Leu Arg Arg
 260 265 270
 Phe Arg Gly Ser Ser Ser Val Val Pro Cys Ala Thr Pro Glu Leu Arg
 275 280 285
 Gln Gly Gln Asp Leu Lys Ser Leu Arg Val Glu Asp Phe Arg Asn Cys
 290 295 300
 Thr Gly Pro Ala Ser Pro His Gln Ile Lys Ser His Thr Leu Ser Thr
 305 310 315 320
 Ser Asp Arg Ala Ala Arg Lys Glu His His Pro Ser His Gly Ala Ser
 325 330 335
 Arg Asp Lys Gly His Pro His Gly His Leu Pro Gly Ser Arg Ser Gly
 340 345 350
 Ser Lys Lys Pro Gly Lys Asn Cys Thr Ser His Arg Asn Arg Asn Gln
 355 360 365
 Ile Ser Lys Gly Ser Ala Gly Lys Glu Leu Pro Glu Leu Gln Asp Tyr
 370 375 380
 Ala Pro Asp Tyr Gln His Lys Phe Ser Phe Asp Ile Met Pro Thr Ala
 385 390 395 400
 Arg Pro Lys Arg Lys Gly Lys Cys Ala Arg Arg Thr Pro Ile Arg Ala
 405 410 415

Pro Ser Gly Val Gln Gln Ala Ser Ser Gly Thr Ala Leu Gly Val Ser		
420	425	430
Leu Leu Ala Trp Ile Leu Gly Leu Val Val Ser Leu Arg		
435	440	445

<210> 10
<211> 473
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 10			
Met Ala Ala Trp Pro Ser Arg Val Gly Ala Trp Arg Pro Gly Ala Gly			
1	5	10	15
Pro Pro Thr Ser Ala Arg Leu Pro Gly Arg Leu Gly Gln Leu Gly Pro			
20	25	30	
Trp Lys Lys Val Gly Cys Cys Val Glu Leu Leu Leu Leu Val Ala			
35	40	45	
Ala Glu Leu Pro Leu Gly Gly Cys Pro Arg Asp Cys Val Cys Tyr			
50	55	60	
Pro Ala Pro Met Thr Val Ser Cys Gln Ala His Asn Phe Ala Ala Ile			
65	70	75	80
Pro Glu Gly Ile Pro Val Asp Ser Glu Arg Val Phe Leu Gln Asn Asn			
85	90	95	
Arg Ile Gly Leu Leu Gln Pro Gly His Phe Ser Pro Ala Met Val Thr			
100	105	110	
Leu Trp Ile Tyr Ser Asn Asn Ile Thr Tyr Ile His Pro Ser Thr Phe			
115	120	125	
Glu Gly Phe Val His Leu Glu Glu Leu Asp Leu Gly Asp Asn Arg Gln			
130	135	140	
Leu Arg Thr Leu Ala Pro Glu Thr Phe Gln Gly Leu Val Lys Leu His			
145	150	155	160
Ala Leu Tyr Leu Tyr Lys Cys Gly Leu Ser Ala Leu Pro Ala Gly Val			
165	170	175	
Phe Gly Gly Leu His Ser Leu Gln Tyr Leu Tyr Leu Gln Asp Asn His			
180	185	190	
Ile Glu Tyr Leu Gln Asp Asp Ile Phe Val Asp Leu Val Asn Leu Ser			
195	200	205	
His Leu Phe Leu His Gly Asn Lys Leu Trp Ser Leu Gly Pro Gly Thr			
210	215	220	
Phe Arg Gly Leu Val Asn Leu Asp Arg Leu Leu His Glu Asn Gln			
225	230	235	240
Leu Gln Trp Val His His Lys Ala Phe His Asp Leu Arg Arg Leu Thr			
245	250	255	
Thr Leu Phe Leu Phe Asn Asn Ser Leu Ser Glu Leu Gln Gly Glu Cys			
260	265	270	
Leu Ala Pro Leu Gly Ala Leu Glu Phe Leu Arg Leu Asn Gly Asn Pro			
275	280	285	
Trp Asp Cys Gly Cys Arg Ala Arg Ser Leu Trp Glu Trp Leu Gln Arg			
290	295	300	
Phe Arg Gly Ser Ser Ala Val Pro Cys Val Ser Pro Gly Leu Arg			
305	310	315	320
His Gly Gln Asp Leu Lys Leu Leu Arg Ala Glu Asp Phe Arg Asn Cys			
325	330	335	

Thr Gly Pro Ala Ser Pro His Gln Ile Lys Ser His Thr Leu Thr Thr
 340 345 350
 Thr Asp Arg Ala Ala Arg Lys Glu His His Ser Pro His Gly Pro Thr
 355 360 365
 Arg Ser Lys Gly His Pro His Gly Pro Arg Pro Gly His Arg Lys Pro
 370 375 380
 Gly Lys Asn Cys Thr Asn Pro Arg Asn Arg Asn Gln Ile Ser Lys Ala
 385 390 395 400
 Gly Ala Gly Lys Gln Ala Pro Glu Leu Pro Asp Tyr Ala Pro Asp Tyr
 405 410 415
 Gln His Lys Phe Ser Phe Asp Ile Met Pro Thr Ala Arg Pro Lys Arg
 420 425 430
 Lys Gly Lys Cys Ala Arg Arg Thr Pro Ile Arg Ala Pro Ser Gly Val
 435 440 445
 Gln Gln Ala Ser Ser Ala Ser Ser Leu Gly Ala Ser Leu Leu Ala Trp
 450 455 460
 Thr Leu Gly Leu Ala Val Thr Leu Arg
 465 470

<210> 11
 <211> 474
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

<400> 11
 Met Leu Pro Gly Leu Arg Arg Leu Leu Gln Gly Pro Ala Ser Ala Cys
 1 5 10 15
 Leu Leu Leu Thr Leu Leu Ala Leu Pro Pro Val Thr Pro Ser Cys Pro
 20 25 30
 Met Leu Cys Thr Cys Tyr Ser Ser Pro Pro Thr Val Ser Cys Gln Ala
 35 40 45
 Asn Asn Phe Ser Ser Val Pro Leu Ser Leu Pro Pro Ser Thr Gln Arg
 50 55 60
 Leu Phe Leu Gln Asn Asn Leu Ile Arg Ser Leu Arg Pro Gly Thr Phe
 65 70 75 80
 Gly Pro Asn Leu Leu Thr Leu Trp Leu Phe Ser Asn Asn Leu Ser Thr
 85 90 95
 Ile Tyr Pro Gly Thr Phe Arg His Leu Gln Ala Leu Glu Glu Leu Asp
 100 105 110
 Leu Gly Asp Asn Arg His Leu Arg Ser Leu Glu Pro Asp Thr Phe Gln
 115 120 125
 Gly Leu Glu Arg Leu Gln Ser Leu His Leu Tyr Arg Cys Gln Leu Ser
 130 135 140
 Ser Leu Pro Gly Asn Ile Phe Arg Gly Leu Val Ser Leu Gln Tyr Leu
 145 150 155 160
 Tyr Leu Gln Glu Asn Ser Leu Leu His Leu Gln Asp Asp Leu Phe Ala
 165 170 175
 Asp Leu Ala Asn Leu Ser His Leu Phe Leu His Gly Asn Arg Leu Arg
 180 185 190
 Leu Leu Thr Glu His Val Phe Arg Gly Leu Gly Ser Leu Asp Arg Leu
 195 200 205
 Leu Leu His Gly Asn Arg Leu Gln Gly Val His Arg Ala Ala Phe His
 210 215 220

Gly Leu Ser Arg Leu Thr Ile Leu Tyr Leu Phe Asn Asn Ser Leu Ala
 225 230 235 240
 Ser Leu Pro Gly Glu Ala Leu Ala Asp Leu Pro Ala Leu Glu Phe Leu
 245 250 255
 Arg Leu Asn Ala Asn Pro Trp Ala Cys Asp Cys Arg Ala Arg Pro Leu
 260 265 270
 Trp Ala Trp Phe Gln Arg Ala Arg Val Ser Ser Asp Val Thr Cys
 275 280 285
 Ala Thr Pro Pro Glu Arg Gln Gly Arg Asp Leu Arg Thr Leu Arg Asp
 290 295 300
 Thr Asp Phe Gln Ala Cys Pro Pro Pro Thr Ser Pro Phe Arg Pro Phe
 305 310 315 320
 Gln Thr Asn Gln Leu Thr Asp Glu Glu Leu Leu Gly Leu Pro Lys Cys
 325 330 335
 Cys Gln Pro Asp Ala Ala Asp Lys Ala Ser Val Leu Glu Pro Gly Arg
 340 345 350
 Pro Ala Ser Ala Gly Asn Ala Leu Lys Gly Arg Val Pro Pro Gly Asp
 355 360 365
 Thr Pro Pro Gly Asn Gly Ser Gly Pro Arg His Ile Asn Asp Ser Pro
 370 375 380
 Phe Gly Thr Leu Pro Gly Ser Ala Glu Pro Pro Leu Thr Ala Leu Arg
 385 390 395 400
 Pro Gly Gly Ser Glu Pro Pro Gly Leu Pro Thr Thr Gly Pro Arg Arg
 405 410 415
 Arg Pro Gly Cys Ser Arg Lys Asn Arg Thr Arg Ser His Cys Arg Leu
 420 425 430
 Gly Gln Ala Gly Ser Gly Ser Ser Gly Thr Gly Asp Ala Glu Gly Ser
 435 440 445
 Gly Ala Leu Pro Ala Leu Ala Cys Ser Leu Ala Pro Leu Gly Leu Ala
 450 455 460
 Leu Val Leu Trp Thr Val Leu Gly Pro Cys
 465 470

<210> 12
 <211> 1425
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

<400> 12
 atgctggcccg ggctccggcg cctgctgcaa ggtcctgcct cagcctgcct cctgctgaca 60
 ctcctggccc tccctcctgt gacccccaggc tgccctatgc tctgcacccg ctactcctct 120
 ccggcccacagg tgagctgcca ggcacaaac ttctcctcg tgccgctgtc cttgccaccc 180
 agtacacaggc gactcttctt gcagaacaac ctcattcgct cactgcggcc aggaactttt 240
 gggcccaacc tgctcacccct gtggctcttc tccaaacaacc tctccaccat ctaccctggc 300
 accttccggcc atctgcaggc cctagagggaa ctggacacctg gtgacaatcg gcacccgtgc 360
 tccctggagc ctgacacccctt ccaggccctg gagaggctgc agtcactaca tctgtaccgg 420
 tgccagctca gcagtctgcc tggcaacatc ttccgaggcc tggtcagccct acagttaccc 480
 tacctccagg agaacaggcct gctccaccta caggatgact tgttcgccga cctggccaac 540
 ctgagccacc ttttcctcca cggaaaccgc ctgcggctgc tcacggagca cgtttccgc 600
 ggcttggca gcctggaccg gctgctgtc cacggaaacc ggctgcaggc cgtagccaccgc 660
 gcagccctcc acggtctcag ccgcctcacc atccttacc tgttcaacaa cagcctggcc 720
 tcgctggccgg gagaggcgct ggctgacccctg ccagcgctcg agttcctgcg gctcaacgc 780
 aacccttggg cgtgcgactg ccgcgcctcg ccgcctctggg cttggttcca gcgccgcgg 840

gtgtccagct	ccgacgtgac	ctgcgccacc	ccgcccggcgc	gccaggccgc	ggacctcgcc	900
acgctgcgcg	acaccgattt	ccaagcgtgc	ccgcccggccca	ctagtcctt	ccgtcccccc	960
cagaccaatc	agctcaactga	tgaggagctg	ctggggcctcc	ccaagtgcgtg	ccagccggat	1020
gctgcagaca	aggcctcagt	actggaaacc	gggaggccgg	cgtctgtgg	aatgcactc	1080
aagggacgtg	tgcctcccg	tgacactcca	ccaggcaatg	gctcaggccc	acggcacatc	1140
aatgactctc	cattttggac	tttgcgggc	tctgcagagc	ccccactgac	tgccctcgcc	1200
cctgggggtt	ccgagccccc	gggactgccc	accacgggtc	cccgccaggag	gccaggttgt	1260
tccagaaaga	accgcaccccg	tagccactgc	cgtctgggc	aggcaggaag	tgggagcagt	1320
ggaactgggg	atgcagaagg	ttcggggggcc	ctgcctgccc	tggcctgcag	ccttgctcct	1380
cttggcccttq	cactqgtact	ttggaccgtg	ctcggggccct	gctga		1425

<210> 13
<211> 420
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 13
 Met Lys Arg Ala Ser Ser Gly Gly Ser Arg Leu Leu Ala Trp Val Leu
 1 5 10 15
 Trp Leu Gln Ala Trp Arg Val Ala Thr Pro Cys Pro Gly Ala Cys Val
 20 25 30
 Cys Tyr Asn Glu Pro Lys Val Thr Thr Ser Cys Pro Gln Gln Gly Leu
 35 40 45
 Gln Ala Val Pro Thr Gly Ile Pro Ala Ser Ser Gln Arg Ile Phe Leu
 50 55 60
 His Gly Asn Arg Ile Ser Tyr Val Pro Ala Ala Ser Phe Gln Ser Cys
 65 70 75 80
 Arg Asn Leu Thr Ile Leu Trp Leu His Ser Asn Ala Leu Ala Gly Ile
 85 90 95
 Asp Ala Ala Ala Phe Thr Gly Leu Thr Leu Leu Glu Gln Leu Asp Leu
 100 105 110
 Ser Asp Asn Ala Gln Leu Arg Val Val Asp Pro Thr Thr Phe Arg Gly
 115 120 125
 Leu Gly His Leu His Thr Leu His Leu Asp Arg Cys Gly Leu Gln Glu
 130 135 140
 Leu Gly Pro Gly Leu Phe Arg Gly Leu Ala Ala Leu Gln Tyr Leu Tyr
 145 150 155 160
 Leu Gln Asp Asn Asn Leu Gln Ala Leu Pro Asp Asn Thr Phe Arg Asp
 165 170 175
 Leu Gly Asn Leu Thr His Leu Phe Leu His Gly Asn Arg Ile Pro Ser
 180 185 190
 Val Pro Glu His Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu
 195 200 205
 Leu His Gln Asn His Val Ala Arg Val His Pro His Ala Phe Arg Asp
 210 215 220
 Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu Ser Met
 225 230 235 240
 Leu Pro Ala Glu Val Leu Val Pro Leu Arg Ser Leu Gln Tyr Leu Arg
 245 250 255
 Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro Leu Trp
 260 265 270
 Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val Pro Cys Asn
 275 280 285

Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg Leu Ala Ala Ser
 290 295 300
 Asp Leu Glu Gly Cys Ala Val Ala Thr Ser Pro Thr Arg Pro Gly Ser
 305 310 315 320
 Arg Ala Arg Gly Asn Ser Ser Ser Asn His Leu Tyr Gly Val Ala Glu
 325 330 335
 Ala Gly Ala Pro Pro Ala Asp Pro Ser Thr Leu Tyr Arg Asp Leu Pro
 340 345 350
 Ala Glu Asp Ser Arg Gly Arg Gln Gly Gly Asp Ala Pro Thr Glu Asp
 355 360 365
 Asp Tyr Trp Gly Gly Tyr Gly Gly Glu Asp Gln Arg Gly Glu Gln Thr
 370 375 380
 Cys Pro Gly Ala Ala Cys Gln Ala Pro Ala Asp Ser Arg Gly Pro Val
 385 390 395 400
 Leu Ser Ala Gly Leu Arg Thr Pro Leu Leu Cys Leu Leu Leu Leu Ala
 405 410 415
 Pro His His Leu
 420

<210> 14
 <211> 1263
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

<400> 14
 atgaagaggg cgtcctccgg aggaagccgg ctgctggcat gggtgttatg gctacaggcc 60
 tggagggtag caacgcctcg ccctggtgcc tgtgtgtgct acaatgagcc caaggtcaca 120
 acaagctgcc cccagcaggg cctgcaggct gtaccactg gcatcccagc ctccagccag 180
 agaatcttcc tgcacggcaa cccaatctct tacgtgccag cggccagctt ccagtcatgc 240
 cggaatctca ccattcctgtg gctgcactca aatgcgtgg ccgggattga tgccgcggcc 300
 ttcactggtc tgaccctcct ggagcaacta gatcttagtg acaatgcaca gctccgtgtc 360
 gtggacccca ccacgttccg tggcctggc cacctgcaca cgctgcaccc agaccgatgc 420
 ggcctgcagg agctggggcc tggcctattc cgtggctgg cagctctgca gtacctctac 480
 ctacaagaca acaacctgca ggcacttccc gacaacaccc tccgagaccc gggcaacctc 540
 acgcattctt ttctgcatgg caaccgtatc cccagtttc ctgagcacgc tttccgtggc 600
 ttgcacagtc ttgaccgtct cctcttgac cagaaccatg tggctgtgt gcacccacat 660
 gcctccggg accttggccg actcatgacc ctctacctgt ttgccaacaa cctctccatg 720
 ctccccgcag aggtcctagt gcccttgagg tctctgcagt acctgcgact caatgacaac 780
 ccctgggtgt gtgactgcag ggcacgtccg ctctgggcct ggctgcagaa gttccgaggt 840
 tcctcatccg aggtgcctcg caacctaccc caacgcctgg caggccgtga tctgaagcgc 900
 ctggctgcca gtgacttaga gggtgtgtct gtggctacta gtcccacgcg gcccggcagc 960
 cgcggccgcg gcaacagctc ttccaaccac ctgtacggcg tggccgaggc gggcgctccc 1020
 cccgcagacc catccacgct ctaccgagac ctgcccgcgg aggactcgcg gggcgctcag 1080
 ggcggggacg cgcccactga ggacgactac tggggggct acggcggcga ggaccagcga 1140
 ggcgagcaga cgtgtcccg ggcgcgtgc caggcgcggc cggactcgcg tggcccccgtg 1200
 ctctcgccg ggctgcgcac ccctctgctc tgccttgc tcctggctcc ccatcacctc 1260
 tga 1263

<210> 15
 <211> 415
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 15

Met	Leu	Arg	Lys	Gly	Cys	Cys	Val	Glu	Leu	Leu	Leu	Leu	Leu	Ala	
1				5				10						15	
Gly	Glu	Leu	Pro	Leu	Ser	Gly	Gly	Cys	Pro	Arg	Asp	Cys	Val	Cys	Tyr
				20				25						30	
Pro	Ser	Pro	Met	Thr	Val	Ser	Cys	Gln	Ala	His	Asn	Phe	Ala	Ala	Ile
				35				40						45	
Pro	Glu	Gly	Ile	Pro	Glu	Asp	Ser	Glu	Arg	Ile	Phe	Leu	Gln	Asn	Asn
				50				55					60		
His	Ile	Thr	Phe	Leu	Gln	Gly	His	Phe	Ser	Pro	Ala	Met	Val	Thr	
				65				70					75	80	
Leu	Trp	Ile	Tyr	Ser	Asn	Asn	Ile	Thr	Phe	Ile	Ala	Pro	Asn	Thr	Phe
				85				90					95		
Glu	Gly	Phe	Val	His	Leu	Glu	Glu	Leu	Asp	Leu	Gly	Asp	Asn	Arg	Gln
				100				105					110		
Leu	Arg	Thr	Leu	Ala	Pro	Glu	Thr	Phe	Gln	Gly	Leu	Val	Lys	Leu	His
				115				120					125		
Ala	Leu	Tyr	Leu	Tyr	Lys	Cys	Gly	Leu	Ser	Ser	Leu	Pro	Ala	Gly	Ile
				130				135					140		
Phe	Gly	Gly	Leu	His	Ser	Leu	Gln	Tyr	Leu	Tyr	Leu	Gln	Asp	Asn	His
				145				150				155		160	
Ile	Glu	Tyr	Leu	Gln	Asp	Asp	Ile	Phe	Val	Asp	Leu	Val	Asn	Leu	Ser
				165				170					175		
His	Leu	Phe	Leu	His	Gly	Asn	Lys	Leu	Trp	Ser	Leu	Gly	Gln	Gly	Ile
				180				185					190		
Phe	Arg	Gly	Leu	Val	Asn	Leu	Asp	Arg	Leu	Leu	His	Glu	Asn	Gln	
				195				200				205			
Leu	Gln	Trp	Val	His	His	Lys	Ala	Phe	His	Asp	Leu	His	Arg	Leu	Thr
				210				215				220			
Thr	Leu	Phe	Leu	Phe	Asn	Asn	Ser	Leu	Thr	Glu	Leu	Gln	Gly	Asp	Cys
				225				230				235		240	
Leu	Ala	Pro	Leu	Val	Ala	Leu	Glu	Phe	Leu	Arg	Leu	Asn	Gly	Asn	Ala
				245				250					255		
Trp	Asp	Cys	Gly	Cys	Arg	Ala	Arg	Ser	Leu	Trp	Glu	Trp	Leu	Arg	Arg
				260				265					270		
Phe	Arg	Gly	Ser	Ser	Ser	Val	Val	Pro	Cys	Ala	Thr	Pro	Glu	Leu	Arg
				275				280					285		
Gln	Gly	Gln	Asp	Leu	Lys	Ser	Leu	Arg	Val	Glu	Asp	Phe	Arg	Asn	Cys
				290				295				300			
Thr	Gly	Pro	Thr	Ser	Pro	Thr	Arg	Pro	Gly	Ser	Arg	Ala	Arg	Gly	Asn
				305				310				315		320	
Ser	Ser	Ser	Asn	His	Leu	Tyr	Gly	Val	Ala	Glu	Ala	Gly	Ala	Pro	Pro
				325				330					335		
Ala	Asp	Pro	Ser	Thr	Leu	Tyr	Arg	Asp	Leu	Pro	Ala	Glu	Asp	Ser	Arg
				340				345					350		
Gly	Arg	Gln	Gly	Gly	Asp	Ala	Pro	Thr	Glu	Asp	Asp	Tyr	Trp	Gly	Gly
				355				360					365		
Tyr	Gly	Gly	Glu	Asp	Gln	Arg	Gly	Glu	Gln	Thr	Cys	Pro	Gly	Ala	Ala
				370				375					380		
Cys	Gln	Ala	Pro	Ala	Asp	Ser	Arg	Gly	Pro	Val	Leu	Ser	Ala	Gly	Leu
				385				390				395		400	
Arg	Thr	Pro	Leu	Leu	Cys	Leu	Leu	Leu	Ala	Pro	His	His	Leu		
				405				410					415		

<210> 16
<211> 1245
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 16

atgcttcgca	aagggtgctg	tgtggaatttgc	ctgctgttgc	tgctggctgg	agagctaccc	60
ctgagtggtg	gttgtcctcg	ctgtgtgtgc	tacccttcgc	ccatgactgt	cagttgccag	120
gcacacaact	ttgcgcgcatt	ccccgagggc	atcccagagg	acagcgagcg	catcttcctg	180
cagaacaatc	acatcacctt	cctccagcag	ggccacttca	gccccgcatt	ggtcaccctc	240
tggatctact	ccaacaacat	cactttcatt	gctcccaaca	cctttgaggg	ctttgtgcat	300
ctggaggagc	tagaccttgg	agacaaccgg	cagcttcgaa	cgctggcacc	cgagaccttc	360
caaggcctgg	tgaagcttca	cgcctctac	ctctacaagt	gcccactgag	ctccctgcct	420
gcgggcatct	ttggtggcct	gcacagcctg	cagtacctt	acttgcagga	caaccatatt	480
gagtacctcc	aagatgacat	ctttgtggac	ctggtcaacc	tcagtcaatt	gtttctccat	540
ggcaacaaggc	tatggagcct	ggccagggc	atcttccggg	gcctggtaa	cctggaccgg	600
ttgctgctgc	atgagaacca	gctacagtgg	gtccaccaca	aggcttcca	tgacactccac	660
aggctaacca	ccctctttct	cttcaacaat	agcctcaccg	agctgcaggg	tgactgcctg	720
gccccccctgg	tggcccttgg	gtttcttcgc	ctcaatggga	atgcttggga	ctgtggctgc	780
cgggcacggt	ccctgtggga	atggctgcga	aggttccgtg	gctccagctc	tgttgtcccc	840
tgcgcgactc	cagagctgctg	gcaaggacag	gacctaagt	cgctgaggg	tgaggacttc	900
cggaaactgca	ctggaccaac	tagtcccacg	cggccgggca	gcccgcggcc	cggcaacagc	960
tcttccaacc	acctgtacgg	cgtggccgag	gcggggcgtc	cccccgca	cccatccacg	1020
ctctaccgag	acctgcccgc	cgaggactcg	cggggcgtc	agggcggggg	cgcgcccact	1080
gaggacgact	actggggggg	ctacggcggc	gaggaccagc	gaggcgagca	gacgtgtccc	1140
ggggccgcgt	gccaggcgcc	cgcggactcg	cgtggccccc	tgctctcggc	cgggctgcgc	1200
accctctgc	tctgccttt	gctcctggct	ccccatcacc	tctga		1245

<210> 17
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 17

Met	Leu	Pro	Gly	Leu	Arg	Arg	Leu	Leu	Gln	Gly	Pro	Ala	Ser	Ala	Cys
1															15
Leu	Leu	Leu	Thr	Leu	Leu	Ala	Leu	Pro	Pro	Val	Thr	Pro	Ser	Cys	Pro
															30
Met	Leu	Cys	Thr	Cys	Tyr	Ser	Ser	Pro	Pro	Thr	Val	Ser	Cys	Gln	Ala
															35
Asn	Asn	Phe	Ser	Ser	Val	Pro	Leu	Ser	Leu	Pro	Pro	Ser	Thr	Gln	Arg
															50
Leu	Phe	Leu	Gln	Asn	Asn	Leu	Ile	Arg	Ser	Leu	Arg	Pro	Gly	Thr	Phe
															65
Gly	Pro	Asn	Leu	Leu	Thr	Leu	Trp	Leu	Phe	Ser	Asn	Asn	Leu	Ser	Thr
															85
Ile	Tyr	Pro	Gly	Thr	Phe	Arg	His	Leu	Gln	Ala	Leu	Glu	Glu	Leu	Asp
															100
															105
															110

Leu Gly Asp Asn Arg His Leu Arg Ser Leu Glu Pro Asp Thr Phe Gln
 115 120 125
 Gly Leu Glu Arg Leu Gln Ser Leu His Leu Tyr Arg Cys Gln Leu Ser
 130 135 140
 Ser Leu Pro Gly Asn Ile Phe Arg Gly Leu Val Ser Leu Gln Tyr Leu
 145 150 155 160
 Tyr Leu Gln Glu Asn Ser Leu Leu His Leu Gln Asp Asp Leu Phe Ala
 165 170 175
 Asp Leu Ala Asn Leu Ser His Leu Phe Leu His Gly Asn Arg Leu Arg
 180 185 190
 Leu Leu Thr Glu His Val Phe Arg Gly Leu Gly Ser Leu Asp Arg Leu
 195 200 205
 Leu Leu His Gly Asn Arg Leu Gln Gly Val His Arg Ala Ala Phe His
 210 215 220
 Gly Leu Ser Arg Leu Thr Ile Leu Tyr Leu Phe Asn Asn Ser Leu Ala
 225 230 235 240
 Ser Leu Pro Gly Glu Ala Leu Ala Asp Leu Pro Ala Leu Glu Phe Leu
 245 250 255
 Arg Leu Asn Ala Asn Pro Trp Ala Cys Asp Cys Arg Ala Arg Pro Leu
 260 265 270
 Trp Ala Trp Phe Gln Arg Ala Arg Val Ser Ser Asp Val Thr Cys
 275 280 285
 Ala Thr Pro Pro Glu Arg Gln Gly Arg Asp Leu Arg Thr Leu Arg Asp
 290 295 300
 Thr Asp Phe Gln Ala Cys Pro Pro Pro Thr Pro Thr Arg Pro Gly Ser
 305 310 315 320
 Arg Ala Arg Gly Asn Thr Ser Pro Gly Arg Pro Ala Ser Ala Gly Asn
 325 330 335
 Ala Leu Lys Gly Arg Val Pro Pro Gly Asp Thr Pro Pro Gly Asn Gly
 340 345 350
 Ser Gly Pro Arg His Ile Asn Asp Ser Pro Phe Gly Thr Leu Pro Gly
 355 360 365
 Ser Ala Glu Pro Pro Leu Thr Ala Leu Arg Pro Gly Gly Ser Glu Pro
 370 375 380
 Pro Gly Leu Pro Thr Thr Gly Pro Arg Arg Arg Pro Gly Cys Ser Arg
 385 390 395 400
 Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly Gln Ala Gly Ser Gly
 405 410 415
 Ser Ser Gly Thr Gly Asp Ala Glu Gly Ser Gly Ala Leu Pro Ala Leu
 420 425 430
 Ala Cys Ser Leu Ala Pro Leu Gly Leu Ala Leu Val Leu Trp Thr Val
 435 440 445
 Leu Gly Pro Cys
 450

<210> 18
 <211> 1359
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

<400> 18
 atgcgtcccg ggctccggcg cctgctgcaa ggtcctgcct cagcctgcct cctgctgaca 60
 ctccctggccc tcccttcctgt gacccccagc tgcccttatgc tctgcacccctg ctactcctct 120

ccgccccacag	ttagctgccca	ggccaacaac	tttcctcgg	tgcgcgtgtc	cttgccaccc	180
agtacacagg	gacttttctt	gcagaacaac	ctcatcgct	cactgcggcc	aggaactttt	240
ggcccaacc	tgctcacccct	gtggctttc	tccaaacaacc	tctccaccat	ctaccctggc	300
accttccgc	atctgcaggc	cctagaggaa	ctggacctcg	gtgacaatcg	gcacctgcgc	360
tccctggagc	ctgacacccct	ccagggcctg	gagaggctgc	agtcaactaca	tctgtaccgg	420
tgccagctca	gcagtctgcc	tggcaacatc	ttccgaggcc	tggtcagcct	acagtacctc	480
tacctccagg	agaacagcct	gctccaccta	caggatgact	tgttcgcccga	cctggccaac	540
ctgagccacc	ttttcctcca	cggaaaccgc	ctgcggctgc	tcacggagca	cgtgtccgc	600
ggcttggca	gcctggaccg	gctgctgtcg	cacgggaacc	ggctgcaggg	cgtacaccgc	660
gcagcattcc	acggtctcag	ccgcctcacc	atccttacc	tgttcaacaa	cagcctggcc	720
tcgctccgg	gagaggcgct	ggctgacctg	ccagcgctcg	agttcctgcg	gctcaacgccc	780
aacccttggg	cgtgcgactg	ccgcgcctcg	ccgcctctggg	cttggttcca	gcccgcgcgg	840
gtgtccagct	ccgacgtgac	ctgcgcacc	ccgcccggagc	gccaggggccg	ggacctgcgc	900
acgctgcgcg	acaccgattt	ccaagcgtgc	ccgcccggcc	caccacgcg	gccggggcagc	960
cgcccccgcg	gcaacactag	tcccgggagg	ccggcgctcg	ctggaaatgc	actcaaggga	1020
cgtgtccctc	ccggtgacac	tccaccaggc	aatggctcg	gcccacggca	catcaatgac	1080
tctccatttg	ggactttgcc	gggctctgca	gagccccac	tgactgcct	gcccgcctggg	1140
ggttccgagc	ccccgggact	gcccaccacg	ggtcccccga	ggaggccagg	ttgttccaga	1200
aagaaccgca	cccgtagcca	ctgccgtctg	ggccaggcag	gaagtgggag	cagtggaaact	1260
ggggatgcag	aaggttcggg	ggccctgcct	gccctggcc	gcagccttgc	tcctctgggc	1320
cttgcactgg	tactttggac	cgtgctcggg	ccctgctga			1359

<210> 19

<211> 441

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 19

Met	Lys	Arg	Ala	Ser	Ser	Gly	Gly	Ser	Arg	Leu	Leu	Ala	Trp	Val	Leu
1				5				10					15		
Trp	Leu	Gln	Ala	Trp	Arg	Val	Ala	Thr	Pro	Cys	Pro	Gly	Ala	Cys	Val
				20				25					30		
Cys	Tyr	Asn	Glu	Pro	Lys	Val	Thr	Thr	Ser	Cys	Pro	Gln	Gln	Gly	Leu
				35				40					45		
Gln	Ala	Val	Pro	Thr	Gly	Ile	Pro	Ala	Ser	Ser	Gln	Arg	Ile	Phe	Leu
				50				55					60		
His	Gly	Asn	Arg	Ile	Ser	Tyr	Val	Pro	Ala	Ala	Ser	Phe	Gln	Ser	Cys
				65				70					75		80
Arg	Asn	Leu	Thr	Ile	Leu	Trp	Leu	His	Ser	Asn	Ala	Leu	Ala	Gly	Ile
				85				90					95		
Asp	Ala	Ala	Ala	Phe	Thr	Gly	Leu	Thr	Leu	Leu	Glu	Gln	Leu	Asp	Leu
				100				105					110		
Ser	Asp	Asn	Ala	Gln	Leu	Arg	Val	Val	Asp	Pro	Thr	Thr	Phe	Arg	Gly
				115				120					125		
Leu	Gly	His	Leu	His	Thr	Leu	His	Leu	Asp	Arg	Cys	Gly	Leu	Gln	Glu
				130				135					140		
Leu	Gly	Pro	Gly	Leu	Phe	Arg	Gly	Leu	Ala	Ala	Leu	Gln	Tyr	Leu	Tyr
				145				150					155		160
Leu	Gln	Asp	Asn	Asn	Leu	Gln	Ala	Leu	Pro	Asp	Asn	Thr	Phe	Arg	Asp
				165				170					175		
Leu	Gly	Asn	Leu	Thr	His	Leu	Phe	Leu	His	Gly	Asn	Arg	Ile	Pro	Ser
				180				185					190		
Val	Pro	Glu	His	Ala	Phe	Arg	Gly	Leu	His	Ser	Leu	Asp	Arg	Leu	Leu

195	200	205
Leu His Gln Asn His Val Ala Arg Val His Pro His Ala Phe Arg Asp		
210	215	220
Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu Ser Met		
225	230	235
Leu Pro Ala Glu Val Leu Val Pro Leu Arg Ser Leu Gln Tyr Leu Arg		
245	250	255
Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro Leu Trp		
260	265	270
Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val Pro Cys Asn		
275	280	285
Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg Leu Ala Ala Ser		
290	295	300
Asp Leu Glu Gly Cys Ala Val Ala Ser Gly Pro Phe Arg Pro Phe Gln		
305	310	315
Thr Asn Gln Leu Thr Asp Glu Glu Leu Leu Gly Leu Pro Lys Cys Cys		
325	330	335
Gln Pro Asp Ala Ala Asp Lys Ala Ser Val Thr Ser Ser Asn His Leu		
340	345	350
Tyr Gly Val Ala Glu Ala Gly Ala Pro Pro Ala Asp Pro Ser Thr Leu		
355	360	365
Tyr Arg Asp Leu Pro Ala Glu Asp Ser Arg Gly Arg Gln Gly Gly Asp		
370	375	380
Ala Pro Thr Glu Asp Asp Tyr Trp Gly Gly Tyr Gly Gly Glu Asp Gln		
385	390	395
Arg Gly Glu Gln Thr Cys Pro Gly Ala Ala Cys Gln Ala Pro Ala Asp		
405	410	415
Ser Arg Gly Pro Val Leu Ser Ala Gly Leu Arg Thr Pro Leu Leu Cys		
420	425	430
Leu Leu Leu Ala Pro His His Leu		
435	440	

<210> 20
<211> 1326
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 20	60
atgaagaggg cgtcctccgg aggaagccgg ctgctggcat gggtgttatg gctacaggcc	120
tggagggtag caacgcctg ccctggtgcc ttgtgtgtct acaatgagcc caaggtcaca	180
acaagctgcc cccagcaggg cctgcaggct gtaccactg gcatacccagc ctccagccag	240
agaatcttcc tgcacggcaa ccgaatctct tacgtgccag cccgcagctt ccagtcatgc	300
cggaatctca ccatcctgtg gctgcactca aatgcgcctgg cccggattga tgccgcggcc	360
ttcactggtc tgaccctcct ggagcaacta gatcttagtg acaatgcaca gctccgtgtc	420
gtggacccca ccacgttccg tggcctgggc cacctgcaca cgctgcacct agaccgatgc	480
ggcctgcagg agctggggcc tggcctattc cgtgggctgg cagctctgca gtacctctac	540
ctacaagaca acaacctgca ggcacttccc gacaacacct tccgagacct gggcaacetc	600
acgcatctct ttctgcatgg caaccgtatc cccagtgttc ctgagcacgc tttccgtggc	660
ttgcacagtc ttgaccgtct cctcttgcac cagaaccatg tggctcggt gcacccacat	720
gcctccggg accttggccg actcatgacc ctctacctgt ttgccaacaa cctctccatg	780
ctccccgcag aggtcctagt gcccctgagg tctctgcagt acctgcgact caatgacaac	840
ccctgggtgt gtgactgcag ggcacgtccg ctctggccct ggctgcagaa gttccgaggt	900
tcctcatccg aggtgcctg caacctaccc caacgcctgg caggccgtga tctgaagcgc	

ctggctgcca	gtgacttaga	gggttgcgt	gtggcttcgg	ggcccttcgg	tcccttcag	960
accaatcagc	tcactgatga	ggagctgctg	ggcctccca	agtgtgcca	gcggatgct	1020
gcagacaagg	cctcagtaac	tagttccaa	cacctgtacg	gcgtggccga	gcggggcgct	1080
ccccccgcag	accatccac	gcttaccga	gacctgccc	ccgaggactc	gcggggcggt	1140
cagggcgggg	acgcgccac	tgaggacgac	tactgggggg	gctacggccgg	cgaggaccag	1200
cgaggcggcgc	agacgtgtcc	cggggccgcg	tgccaggcgc	ccgeggactc	gcgtggcccc	1260
gtgctctcgg	ccgggctgcg	caccctctg	ctctgcctct	tgctcctggc	tccccatcac	1320
					ctctga	1326

<210> 21
<211> 452
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 21						
Met Lys Arg Ala Ser Ser Gly Gly Ser Arg Leu Leu Ala Trp Val Leu						
1	5	10	15			
Trp Leu Gln Ala Trp Arg Val Ala Thr Pro Cys Pro Gly Ala Cys Val						
20	25	30				
Cys Tyr Asn Glu Pro Lys Val Thr Thr Ser Cys Pro Gln Gln Gly Leu						
35	40	45				
Gln Ala Val Pro Thr Gly Ile Pro Ala Ser Ser Gln Arg Ile Phe Leu						
50	55	60				
His Gly Asn Arg Ile Ser Tyr Val Pro Ala Ala Ser Phe Gln Ser Cys						
65	70	75	80			
Arg Asn Leu Thr Ile Leu Trp Leu His Ser Asn Ala Leu Ala Gly Ile						
85	90	95				
Asp Ala Ala Ala Phe Thr Gly Leu Thr Leu Leu Glu Gln Leu Asp Leu						
100	105	110				
Ser Asp Asn Ala Gln Leu Arg Val Val Asp Pro Thr Thr Phe Arg Gly						
115	120	125				
Leu Gly His Leu His Thr Leu His Leu Asp Arg Cys Gly Leu Gln Glu						
130	135	140				
Leu Gly Pro Gly Leu Phe Arg Gly Leu Ala Ala Leu Gln Tyr Leu Tyr						
145	150	155	160			
Leu Gln Asp Asn Asn Leu Gln Ala Leu Pro Asp Asn Thr Phe Arg Asp						
165	170	175				
Leu Gly Asn Leu Thr His Leu Phe Leu His Gly Asn Arg Ile Pro Ser						
180	185	190				
Val Pro Glu His Ala Phe Arg Gly Leu His Ser Leu Asp Arg Leu Leu						
195	200	205				
Leu His Gln Asn His Val Ala Arg Val His Pro His Ala Phe Arg Asp						
210	215	220				
Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu Ser Met						
225	230	235	240			
Leu Pro Ala Glu Val Leu Val Pro Leu Arg Ser Leu Gln Tyr Leu Arg						
245	250	255				
Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro Leu Trp						
260	265	270				
Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val Pro Cys Asn						
275	280	285				
Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg Leu Ala Ala Ser						
290	295	300				

Asp Leu Glu Gly Cys Ala Val Ala Thr Ser Pro Thr Arg Pro Gly Ser
 305 310 315 320
 Arg Ala Arg Gly Asn Thr Ser Pro Gly Arg Pro Ala Ser Ala Gly Asn
 325 330 335
 Ala Leu Lys Gly Arg Val Pro Pro Gly Asp Thr Pro Pro Gly Asn Gly
 340 345 350
 Ser Gly Pro Arg His Ile Asn Asp Ser Pro Phe Gly Thr Leu Pro Gly
 355 360 365
 Ser Ala Glu Pro Pro Leu Thr Ala Leu Arg Pro Gly Gly Ser Glu Pro
 370 375 380
 Pro Gly Leu Pro Thr Thr Gly Pro Arg Arg Arg Pro Gly Cys Ser Arg
 385 390 395 400
 Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly Gln Ala Gly Ser Gly
 405 410 415
 Ser Ser Gly Thr Gly Asp Ala Glu Gly Ser Gly Ala Leu Pro Ala Leu
 420 425 430
 Ala Cys Ser Leu Ala Pro Leu Gly Leu Ala Leu Val Leu Trp Thr Val
 435 440 445
 Leu Gly Pro Cys
 450

<210> 22

<211> 1359

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 22

atgaagaggg	cgtcctccgg	aggaagccgg	ctgctggcat	gggtgttatg	gctacaggcc	60
tggagggtag	caacgcctg	ccctggtgcc	tgtgtgtgct	acaatgagcc	caaggtcaca	120
acaagctgcc	cccagcaggg	cctgcaggct	gtaccactg	gcatcccagc	ctccagccag	180
agaatcttcc	tgcacggcaa	cgaatctct	tacgtgccag	ccgcccagctt	ccagtcatgc	240
cggaatctca	ccatcctgtg	gctgcactca	aatgcgtctgg	ccgggattta	tgccgcggcc	300
ttcactggtc	tgaccctcct	ggagcaacta	gatcttagtg	acaatgcaca	gctccgtgtc	360
gtggacccca	ccacgttccg	tggcctgggc	cacctgcaca	cgctgcaccc	agaccgatgc	420
ggcctgcagg	agctggggcc	tggcctattc	cgtggctgg	cagctctgca	gtacctctac	480
ctacaagaca	acaacctgca	ggcacattcc	gacaacaccc	tccgagaccc	ggcaacacct	540
acgcatctct	ttctgcatgg	caaccgtatac	cccagtgttc	ctgagcacgc	tttccgtggc	600
ttgcacagtc	ttgaccgtct	cctcttgac	cagaaccatg	tggctcgat	gcacccacat	660
gccttccggg	accttggccg	actcatgacc	ctctacctgt	ttgccaacaa	cctctccatg	720
ctccccgcag	aggtcctagt	gcccttgagg	tctctgcagt	acctgcgact	aatgacaac	780
ccctgggtgt	gtgactgcag	ggcacgtccg	ctctggccct	ggctgcagaa	gttccgaggt	840
tcctcatccg	aggtgccctg	caacctaccc	caacgcctgg	caggccgtga	tctgaagcgc	900
ctggctgcca	gtgacttaga	gggttgtgct	gtggctacta	gacccacgcg	gccgggcagc	960
cgcggccgcg	gcaacactag	tcccgggagg	ccggcgtctg	ctggaaatgc	actcaaggga	1020
cgtgtgcctc	ccggtgacac	tccaccaggc	aatggctcag	gcccacggca	catcaatgac	1080
tctccatttg	ggactttgcc	gggctctgca	gagccccccac	tgactgcct	gcggcctggg	1140
ggttccgagc	ccccgggact	gcccaccacg	ggtccccgca	ggaggccagg	ttgttccaga	1200
aagaaccgca	cccgtagcca	ctgccgtctg	ggccaggcag	gaagtgggag	cagtggact	1260
ggggatgcag	aaggttccggg	ggccctgcct	gcccctggct	gcagccttgc	tcctctgggc	1320
cttgcaactgg	tactttggac	cgtgctcgaa	ccctgctga			1359

<210> 23

<211> 452

<212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:/Note =
 Synthetic Construct

<400> 23
 Met Leu Pro Gly Leu Arg Arg Leu Leu Gln Gly Pro Ala Ser Ala Cys
 1 5 10 15
 Leu Leu Leu Thr Leu Leu Ala Leu Pro Pro Val Thr Pro Ser Cys Pro
 20 25 30
 Met Leu Cys Thr Cys Tyr Ser Ser Pro Pro Thr Val Ser Cys Gln Ala
 35 40 45
 Asn Asn Phe Ser Ser Val Pro Leu Ser Leu Pro Pro Ser Thr Gln Arg
 50 55 60
 Leu Phe Leu Gln Asn Asn Leu Ile Arg Ser Leu Arg Pro Gly Thr Phe
 65 70 75 80
 Gly Pro Asn Leu Leu Thr Leu Trp Leu Phe Ser Asn Asn Leu Ser Thr
 85 90 95
 Ile Tyr Pro Gly Thr Phe Arg His Leu Gln Ala Leu Glu Glu Leu Asp
 100 105 110
 Leu Gly Asp Asn Arg His Leu Arg Ser Leu Glu Pro Asp Thr Phe Gln
 115 120 125
 Gly Leu Glu Arg Leu Gln Ser Leu His Leu Tyr Arg Cys Gln Leu Ser
 130 135 140
 Ser Leu Pro Gly Asn Ile Phe Arg Gly Leu Val Ser Leu Gln Tyr Leu
 145 150 155 160
 Tyr Leu Gln Glu Asn Ser Leu Leu His Leu Gln Asp Asp Leu Phe Ala
 165 170 175
 Asp Leu Ala Asn Leu Ser His Leu Phe Leu His Gly Asn Arg Leu Arg
 180 185 190
 Leu Leu Thr Glu His Val Phe Arg Gly Leu Gly Ser Leu Asp Arg Leu
 195 200 205
 Leu Leu His Gly Asn Arg Leu Gln Gly Val His Arg Ala Ala Phe His
 210 215 220
 Gly Leu Ser Arg Leu Thr Ile Leu Tyr Leu Phe Asn Asn Ser Leu Ala
 225 230 235 240
 Ser Leu Pro Gly Glu Ala Leu Ala Asp Leu Pro Ala Leu Glu Phe Leu
 245 250 255
 Arg Leu Asn Ala Asn Pro Trp Ala Cys Asp Cys Arg Ala Arg Pro Leu
 260 265 270
 Trp Ala Trp Phe Gln Arg Ala Arg Val Ser Ser Asp Val Thr Cys
 275 280 285
 Ala Thr Pro Pro Glu Arg Gln Gly Arg Asp Leu Arg Thr Leu Arg Asp
 290 295 300
 Thr Asp Phe Gln Ala Cys Pro Pro Pro Thr Pro Thr Arg Pro Gly Ser
 305 310 315 320
 Arg Ala Arg Gly Glu Thr Ser Pro Gly Arg Pro Ala Ser Ala Gly Asn
 325 330 335
 Ala Leu Lys Gly Arg Val Pro Pro Gly Asp Thr Pro Pro Gly Asn Gly
 340 345 350
 Ser Gly Pro Arg His Ile Asn Asp Ser Pro Phe Gly Thr Leu Pro Gly
 355 360 365
 Ser Ala Glu Pro Pro Leu Thr Ala Leu Arg Pro Gly Gly Ser Glu Pro
 370 375 380
 Pro Gly Leu Pro Thr Thr Gly Pro Arg Arg Pro Gly Cys Ser Arg

385	390	395	400
Lys Asn Arg Thr Arg Ser His Cys Arg Leu Gly Gln Ala Gly Ser Gly			
405	410	415	
Ser Ser Gly Thr Gly Asp Ala Glu Gly Ser Gly Ala Leu Pro Ala Leu			
420	425	430	
Ala Cys Ser Leu Ala Pro Leu Gly Leu Ala Leu Val Leu Trp Thr Val			
435	440	445	
Leu Gly Pro Cys			
450			

<210> 24

<211> 1358

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 24

atgctgccccg ggctccggcg cctgctgcaa ggtcctgcct cagcctgcct cctgctgaca	60
ctccctggccc tcccttcgtt gaccccccagc tgcccttatgc tctgcacccg ctactcctct	120
ccgccccacag tgagctgcca ggccaacaac ttcttcctcg tgccgctgtc cttgccaccc	180
agtacacacgc gactttttt gcagaacaac ctcattcgct cactgcggcc aggaactttt	240
gggcccccaacc tgctcacccct gtggctcttc tccaaacaacc tctccaccat ctaccctggc	300
accttcggcc atctgcaggc ccttagaggaa ctggacccctcg gtgacaatcg gcacctgcgc	360
tccctggagc ctgacacccctt ccaggccctcg gagaggctgc agtcaactaca tctgtaccgg	420
tgccagctca gcagtctgcc tggcaacatc ttccgaggcc tggtcagccct acagtaccc	480
taccccccagg agaacagcct gctccaccta caggatgact tggccggccga cctggccaac	540
ctgagccacc ttttcctcca cgggaaccgc ctgcggctgc tcacggagca cgtgttccgc	600
ggcttggca gcctggaccg gctgctgtc cacgggaacc gcgtgcaggc cgtaacccgc	660
gcagccctcc acggtctcag ccgcctcacc atccttacc tggcaacaa cagcctggcc	720
tgcgtccgg gagaggccgt ggcgtacccg ccagcgtcg agttcctgcg gctcaacgccc	780
aaccctggg cgtgcgactg ccgcgtctgg ccgcctctggg cttgggttcca gcgcgcgcgg	840
gtgtccagct ccgacgtgac ctgcggccacc ccgcggcagc gccaggccgg ggacctgcgc	900
acgctgcgcg acaccgattt ccaaggcgtgc ccgcggccca caccacgcg gcccggcagc	960
cgcggccgcg ggaaactagt cccgggaggc cggcgtctgc tggaaatgca ctcaaggagc	1020
gtgtccctcc cggtgacact ccaccaggca atggctcagg cccacggcac atcaatgact	1080
ctccatattgg gactttggccg ggctctgcag agcccccaact gactgcctcg cggcctgggg	1140
gttccgagcc cccgggactg cccaccacgg gtcccgccag gaggccaggt tggccatggaa	1200
agaacccgcac ccgtagccac tgccgtctgg gccaggcagg aagtgggagc agtggaaactg	1260
gggatgcaga agttcgggg gcctgcctg ccctgcctg cagccttgcg cctctggcc	1320
ttgcaactggc actttggacc gtgctcgggc cctgctga	1358

<210> 25

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 25

Thr Gly Pro Arg Arg Pro Gly Cys Ser Arg Lys Asn Arg Thr Arg			
1	5	10	15
Leu			

<210> 26
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 26
Thr Ala Arg Pro Lys Arg Lys Gly Lys Cys Ala Arg Arg Thr
1 5 10

<210> 27
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 27
His Ser Gly Ala Gly
1 5

<210> 28
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 28
gccatcccg agggcatccc 20

<210> 29
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/Note =
Synthetic Construct

<400> 29
acacttatacg aggttagaggg cgtg 24